Figure 1:

Comparison of the predicted amino acid sequence of the *T. aureum* probe 'TA-PKS-1-consensus' and the homologous region on ORF A of *Schizochytrium* PKS gene cluster (Accession number AAK72879).

```
Quality:    1269              Length:     525
Ratio:  2.469                 Gaps:       10
Percent Similarity: 61.690    Percent Identity: 52.849

        Match display thresholds for the alignment(s):
                | = IDENTITY
                : =    2
                . =    1

TA-PKS-1-consensus.pep x aak72879.genpept..


   1 LCKTLDLEWPH..VFARSIDIELGANEETAAQAIFEELSCPDLTVREAGY 48
     ||||: |||    ||.| :|| | . | || ||  |:.| |: :|| |
2277 LCKTIGLEWSESDVFSRGVDIAQGMHPEDAAVAIVREMACADIRIREVGI 2326

  49 TKDGKRWTTEARPVGLGKPKQALRSSDVFLVSGGARGITPVCVRELAKSI 98
     . .| |  |  .  | |.. :   || ||||||||||.|:||: : |
2327 GANQQRCTIRAAKLETGNPQRQIAKDDVLLVSGGARGITPLCIREITRQI 2376

  99 SGGTFVLLGRSPL.ADDPAWACGV.EEANIGTAAMAHLKAEFAAGRGPKP 146
     .|| ::||||| . | :||| |: :|  : ||   ||  |.|| ||||
2377 AGGKYILLGRSKVSASEPAWCAGITDEKAVQKAATQELKRAFSAGEGPKP 2426

 147 TPKAHKALVGSVLGAREVLGSLESIRAQGARAEYVSCDVSCAERVKAVVD 196
     ||:|    ||||||||||||||||| |: .| | | :| | ||||. | |    |
2427 TPRAVTKLVGSVLGAREVRSSIAAIEALGGKAIYSSCDVNSAADVAKAVR 2476

 197 DLERRVGA.VTGVVHASGVLRDKSVERLELADFEVVYGTKVDGLLNLLQA 245
     | |  ..|| |.|:|||||||||: :|:    :|: |:|||| || ||| |
2477 DAESQLGARVSGIVHASGVLRDRLIEKKLPDEFDAVFGTKVTGLENLLAA 2526

 246 VDRPKLRHLVLFSSLAGFHGNTGQAVYAMANEALNKMAFHLETAMPGLSV 295
     |||   |:|:||||||||||||||||||.||. ||||||||||    || |   .||
2527 VDRANLKHMVLFSSLAGFHGNVGQSDYAMANEALNKMG..LELA.KDVSV 2573

 296 KTIGFGPWDGGMVNDALKAHFASMGVQIIPLDGGAETVSRIIGACSPTQV 345
     |.| |||||||||    || |  ||||||| :|||:||.|.|:    || ::
2574 KSICFGPWDGGMVTPQLKKQFQEMGVQIIPREGGADTVARIVLGSSPAEI 2623

 346 LVGNWGLPPVVPNASVHKITVRLGGESANPFLSSHTIQGRKVLPMTXALG 395
     ||||| |   .   : :: .| |||| | ||||:|||| |:|
2624 LVGNWRTPSKKVGSDTITLHRKISAKS.NPFLEDHVIQGRRVLPMTLAIG 2672
```

```
 396 LLAEAARGLYVGHQVXGIEDAQVFQGVVLDKGATCEVQLRRESSTASPSE 445
     |||    ||: |: .   |:|||.|.|| .|    ||| |    |||
2673 SLAETCLGLFPGYSLWAIDDAQLFKGVTVDGDVNCEVTL..TPSTAPSGR 2720

 446 VVLSASLNVFAAGKVVPAYRAHVVLGASGPRTGGVQLELKDLGVDADPAC 495
     | . |.|  |..||.||||||| :||   |      ::   |  |||||
2721 VNVQATLKTFSSGKLVPAYRAVIVLSNQGAPPANATMQPPSL..DADPAL 2768

 496 SVGKGALYDGRTLFHGPAFQYMDEV 520
       .|..|||:||||||||. .|:|
2769 ...QGSVYDGKTLFHGPAFRGIDDV 2790
```

Figure 2:

Comparison of the predicted amino acid sequence of the *T. aureum* probe 'TA-PKS-1-consensus' and the homologous region on ORF 5 of *Shewanella* PKS gene cluster (Accession number AAB81123).

```
Quality:     641          Length:     551
Ratio:  1.233             Gaps:       16
Percent Similarity: 47.379   Percent Identity: 39.919

        Match display thresholds for the alignment(s):
                    | = IDENTITY
                    : =    2
                    . =    1


TA-PKS-1-consensus.pep x aab81123.genpept


   1 LCKTLDLEWPHVFARSIDIELGANEETAAQAIFEELSCPDLTVREAGYTK 50
     | ||| ||| || |.:||       .    | || ||      . | | .
2094 LTKTLSHEWPQVFCRALDIATDVDATHLADAITSELFDSQAQLPEVGLSL 2143

  51 .DGK..RWTTEARPVGLGKPKQALRSSDVFLVSGGARGITPVCVRELAKS 97
     |||  | |    |        | | |.| ||.|||:|:|  |   || |
2144 IDGKVNRVTLVAAEAADKTAKAELNSTDKILVTGGAKGVTFECALALA.S 2192

  98 ISGGTFVLLGRSPLADDPAWACGVEEANIGTAAMAHLKAEFAAGRGPKPT 147
     |    |:| ||| |      |.|| |  :  : .||.||:        | |||
2193 RSQSHFILAGRSELQALPSWAEGKQTSELKSAAIAHI.....ISTGQKPT 2237

 148 PKAHKALVGSVLGAREVLGSLESIRAQGARAEYVSCDVSCAERVKAVVDD 197
     ||  .| |  |    . |:  .| .    || ||||| ||. .  : |
2238 PKQVEAAVWPVQSSIEINAALAAFNKVGASAEYVSMDVTDSAAITAA... 2284

 198 LERRVGAVTGVVHASGVLRDKSVERLELADFEVVYGTKVDGLLNLLQAVD 247
     | |   :||.:| .||| || ::   ||:    ||||||.|| || |.:
2285 LNGRSNEITGLIHGAGVLADKHIQDKTLAELAKVYGTKVNGLKALLAALE 2334

 248 RPKLRHLVLFSSLAGFHGNTGQAVYAMANEALNKMAFHLETAMPGLSVKT 297
     |:: | :||| |||:|| ||. |||.|: ||| |       |   | .
2335 PSKIKLLAMFSSAAGFYGNIGQSDYAMSNDILNKAALQFTARNPQAKVMS 2384

 298 IGFGPWDGGMVNDALKAHFASMGVQIIPLDGGAETVSRIIGACSPTQVLV 347
     .||||||||| |||  |   || :||| |||  .  : | .  |.|:
2385 FNWGPWDGGMVNPALKKMFTERGVYVIPLKAGAELFATQLLAETGVQLLI 2434

 348 G....................NWG..LPPVVPNASVHK......IT.VRLG 369
     |                    | |  | |    | |   | |    :|  ||
2435 GTSMQGGSDTKATETASVKKLNAGEVLSASHPRAGAQKTPLQAVTATRLL 2484

 370 GESANPFLSSHTIQGRKVLPMTXALGLLAEAARGLYVGHQVXGIEDAQVF 419
     || |: | | | ||| |: : |||  : .| || : | ..
```

```
2485  TPSAMVFIEDHRIGGNSVLPTVCAIDWMREAASDM.LGAQVK.VLDYKLL  2532
              .         .         .         .         .
 420  QGVVLDKGATCEVQLRRESSTASPSEVVLSASLNVFAAGKVVPAYRAHVV  469
      .|:|  :       |. |  | .     |  | | :.    |:  | |:| .:
2533  KGIVFETDEPQELTL..ELTPDDSDEATLQALIS..CNGR..PQYKATLI  2576
              .         .         .         .         .
 470  LGASGPRTGGVQLELKDLGVDADPACSVGKGALYDGRTLFHGPAFQYMDE  519
        .   :    | :|      .  | . | ||   ||||||  | .
2577  SDNADIKQLNKQFDL......SAKAITTAK.ELYSNGTLFHGPRLQGIQS  2619

 520  V 520
      |
2620  V 2620
```
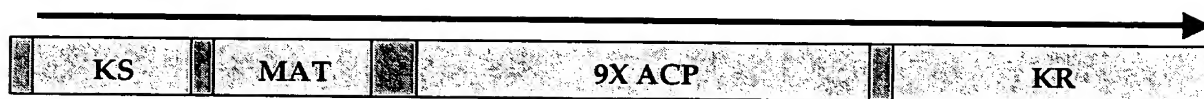
Figure 3:

Organization of PUFA-PKS genes from *Thraustochytrium aureum* ATCC 34304

ORF A- 8748 bp

ORF B- 6123 bp

KS= β-keto acyl synthase

MAT= MalonylCoA

transferase

ACP= Acyl carrier protein

KR= Ketoacyl-ACP reductase

AT= Acyl transferase

FIGURE 4

Sequence ID Nos. and Corresponding Sequences:

SEQ ID NO 1:

5'-AGC GGA TAA CAA TTT CAC ACA GG-3'

SEQ ID NO 2:

CACGAGGCCAAGCATTCGAGCAAAGCGCTCAACCAGCAGATCCCAGG

CGGGCGCGCCTGCTTCGTGGGCGTCTCGCGAATCGACGGACAGCTCG

GACTTAGCGGAGCTTGCGCGAAAGGAAAGGGCTGGGCTGAGGCCGCA

GAGATTGCTCAGCAAGGAGCCGTCGCAGGCTTGTGCAAGACCTTGGA

CCTAGAGTGGCCGCACGTCTTCGCTCGCAGCATCGACATCGAGCTTGG

CGCGAACGAAGAAACAGCTGCGCAAGCAATCTTTGAGGAGCTCTCTT

GCCCGGACCTAACGGTGCGCGAAGCAGGATACACCAAAGACGGCAA

GCGGTGGACGACTGAGGCGCGACCGGTTGGGCTTGGCAAGCCCAAGC

AGGCACTACGTTCTTCGGACGTCTTCTTGGTTTCTGGTGGGGCGCGGGG

AATTACACCTGTTTGCGTTCGCGAGTTGGCCAAATCGATCAGTGGTGG

CACTTTTGTCCTCCTCGGGCGGTCCCCTCTCGCTGATGATCCGGCGTGG

GCTTGCGGCGTCGAGGAAGCAAACATTGGGACAGCCGCTATGGCGCA

CCTCAAGGCCGAGTTCGCAGCCGGGCGCGGCCCGAAGCCGACGCCAA

AGGCCCACAAAGCACTCGTTGGGAGCGTCCTGGGGGCGCGCGAAGTC

CTTGGTTCGCTAGAGAGTATTCGCGCCCAGGGTGCGCGCGCCGAGTAC

GT

SEQ ID NO:3:

TCGCCAACACAAGTTCTGGTTGGCAACTGGGGCTTGCCCCCTGTAGTT

CCTAACGCGAGCGTGCACAAGATTACTGTGAGGCTTGGCGGGGAGTC

TGCAAACCCTTTCCTGTCCTCCCACACGATTCAAGGCAGAAAGGTCTT

GCCGATGACTGYGGCGCTTGGGCTTCTCGCTGAGGCGGCTCGAGGGCT

CTACGTCGGTCACCAAGTAGYCGGGATTGAGGACGCCCAAGTCTTCCA

GGGAGTCGTGTTGGACAAAGGGGCGACGTGTGAGGTCCAGCTTCGCC

GCGAGTCTTCGACTGCAAGCCCAAGCGAGGTTGTGCTGAGTGCTTCGC

TCAATGTATTCGCGGCGGGAAAGGTTGTGCCTGCGTACCGCGCGCATG

TCGTGCTCGGCGCTTCAGGGCCACGCACTGGCGGCGTGCAGCTTGAAC

TGAAAGATTTGGGCGTGGACGCCGACCCTGCTTGCTCCGTTGGCAAGG

GTGCGCTGTACGACGGTAGGACGCTGTTCCATGGGCCGGCGTTTCAGT

ACATGGATGAGGTTCCCTGGTGCTCGCCTGCAGAGCTTGCCGTGCGGT

GCCGTGTCGTTCCGAGCGCGGCTCAGGACCGCGGCCAATATGTTTCGC

GCGGAGTGTTGTACGACCCGTTCCTGAACGACACGGTGTTTCAAGCTC

TCCTTGTTTGGGCCCGTCTGGTCAGGGACAGCGCTTCGCTACCGAGCA

ACGTTGAACGAATCTCGTTCCACGGCCAGCCGCCGAGCGAGGGCGAG

GTGTAGTACACCACGCTCAAGCTGGACAGTGCTGCGAGCGGGCCGCT

CGACCCGATTGCAACAGGCGCATTTCTTCCTCCACCGAGCTTGCGGGG

CGGTCTTTGCATCAGGGCGAGCGAGTGTGGTTCTGAACAAGGCTCTTT

CGTATGATGGCTCTCGACCCAAAGGCGAGTAGAGTACTCTACTCAGTA

CTCCTTTTCACATACCGGCAGGCAGCGTTGCTGTGGGATGGCCGGGGG

CTCTTCTGCACGCGGCTCC

SEQ ID NO: 4:

GAATTCGGCACGAGGCCGGCCTCACGACGCAGGTTGTTCGGTTCCGCG

CTGCAGGTCTGTCACGCAACGCGGACGGCTCTGTTCGAGTCCGCAACC

GCATCATCGGAAAGATTTCGCGCACGGAGCTCGCGGAGATGTTCATTC

GCCCCGCTCCGGAGGCCCTCTTGACCAAGTTGGTTGCGTCGGGTGAGA

TTTCGGCCGAGCAGMNGCCTGGCCAAACAAGTGCCGATGCCGACGAC

ATTGCCGTCGAGSAGAACTCGGGCGGCCACACGGACAATCGCCCGAT

CCATGTCATCCTTCCGCTGATCATCGCGCTCCGCAACAGGCTGCACAA

GGAGTGCGGTTACCCGGCGAGCCTTCGCGTTCGAGTTGGCGCGGGTGG

CGGGATCGGCTGCCCGCTTGCAGCAACTGCGGCCTTCAACATGGGCGC

CGCCTTTCTCGTGACAGGAACAGTCAACCAACTCAGCCGGCAGTCGG

GCACCTGCGACGCGGTGCGCATSAGCTTTTCAAAAGCGACCTACTCGG

ACATCACAATGGCGCCCGCCGCAGATATGTTTGACCAGGGGGTTGAG

CTCCAGGTGCTCAAGAAGGGCACCATGTTTCCGTCGCGCGCCAAGAA

GCTCTACGAGCTGTTTTGCACGTACAACTCGKTCGACGAGATGCCCGC

CGAGGAGCTCGCGCGGGTTGAGAAGCSGATYTTCCAAAAGCCCCTCG

CGGSCGTATGGGACGAGACGAAAGACTTTTACATCAACCGTCTCCACA

ACGAGGACAAGATCGAACGCGCAGAAAGGATGGCAAGCTCAAGAT

GTCGCTCTCGTTCCGCTGGTACCTTGGCCTGAGTTCGTTCTGGGCCAAC

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GCGATTGGGGCCTGGAACGACTTTGCCAAGGGATCCTACCTCGACGCC

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CTCCACGCGCGGCCTACATGCAGCGCCTTCTGGCCGTCAAGCATGACC

CGCGCATCGAGTTTGACCTCGAGGACCCGGTCTTTGGTACGCCCCCAC

TGCCGCGCTCTAAAGCGATGCAGCAACGCACTCTTTCGGAGGCCCGTC

GCTGCAGCACTTGTGCGAACTCGATAGGGTTTCTTTCAAGATTTCAATC

AACAAAACAAGTATTGGAATGACAAAAAAAAAAAAAAAAAACTCGAG

SEQ ID NO:5:

5'- CTT GTG CAA GAC CTT GGA CCT AGA G-3'

SEQ ID NO:6:

5'-GAA CCT CAT CCA TGT ACT GAA ACG C-3'

SEQ ID NO:7:

TTGTGCAAGA CCTTGGACCT AGAGTGGCCG CACGTCTTCG

CTCGCAGCATCGACATCGAG CTTGGCGCGA ACGAAGAAAC

AGCTGCGCAA GCAATCTTTGAGGAGCTCTC TTGCCCGGAC

CTAACGGTGC GCGAAGCAGG ATACACCAAAGACGGCAAGC

GGTGGACGAC TGAGGCGCGA CCGGTTGGGC TTGGCAAGCC

CAAGCAGGCA CTACGTTCTT CGGACGTCTT CTTGGTTTCT

GGTGGGGCGCGGGGAATTAC ACCTGTTTGC GTTCGCGAGT

TGGCCAAATC GATCAGTGGTGGCACTTTTG TCCTCCTCGG

 GCGGTCCCCT CTCGCTGATG ATCCGGCGTGGGCTTGCGGC

GTCGAGGAAG CAAACATTGG GACAGCCGCT ATGGCGCACC

TCAAGGCCGA GTTCGCAGCC GGGCGCGGCC CGAAGCCGAC

GCCAAAGGCCCACAAAGCAC TCGTTGGGAG CGTCCTGGGG

GCGCGCGAAG TCCTTGGTTCGCTAGAGAGT ATTCGCGCCC

AGGGTGCGCG CGCCGAGTAC GTTTCCTGCGACGTTTCGTG

TGCGGAGCGC GTCAAGGCCG TCGTCGACGA TCTCGAGCGA

CGGGTCGGGG CTGTAACTGG GGTTGTGCAC GCCTCTGGTG

TTCTCCGAGACAAGTCCGTT GAGCGCTTGG AGCTCGCCGA

CTTCGAGGTC GTGTACGGCACCAAGGTGGA CGGCCTGCTC

AACCTGCTGC AGGCCGTGGA CCGCCCCAAACTCCGGCACT

TGGTCCTCTT CAGCTCCCTG GCCGGTTTCC ACGGCAACAC

TGGGCAGGCC GTGTACGCTA TGGCGAATGA GGCGCTGAAC

AAGATGGCCTTCCATTTGGA AACTGCGATG CCTGGCCTCT

CGGTCAAGAC GATCGGGTTTGGACCTTGGG ACGGCGGCAT

GGTCAACGAT GCGCTGAAAG CGCACTTTGCGTCTATGGGC

GTCCAAATTA TTCCGCTCGA CGGYGGCGCG GAGACCGTTT

CCCGAATCAT CGGGGCGTGC TCGCCAACAC AAGTTCTGGT

TGGCAACTGGGGCTTGCCCC CTGTAGTTCC TAACGCGAGC

GTGCACAAGA TTACTGTGAGGCTTGGCGGG GAGTCTGCAA

ACCCTTTCCT GTCCTCCCAC ACGATTCAAGGCAGAAAGGT

CTTGCCGATG ACTGYGGCGC TTGGGCTTCT CGCTGAGGCG

GCTCGAGGGC TCTACGTCGG TCACCAAGTA GYCGGGATTG

AGGACGCCCAAGTCTTCCAG GGAGTCGTGT TGGACAAAGG

GGCGACGTGT GAGGTCCAGCTTCGCCGCGA GTCTTCGACT

GCAAGCCCAA GCGAGGTTGT GCTGAGTGCTTCGCTCAATG

TATTCGCGGC GGGAAAGGTT GTGCCTGCGT ACCGCGCGCA

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CTTGCTCCGT TGGCAAGGGTGCGCTGTACG ACGGTAGGAC

GCTGTTCCAT GGGCCGGCGT TTCAGTACATGGATGAGGTT C

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ATACTGCCTTGCGGTGAGTCAGTGCGCGAGTCGTGGGAGGCGATTCGC

GAGGGGCTCGATTGCCTGCAGGACCTGCCTGCGGACCGAGTCGATAT

CACGGCGTACTACGACCCGAACAAGACAACCAAGGACAAGATCTACT

GCAAGCGCGGCGGCTTCATTCCCGAGTATGACTTTGACGCGCGCGAGT

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GCGTGCGCCAGCTCGCTCATCGCGATCAAGGTTGCCATTGATGAGCTC

CTCCACGGGGACTGCGACACCATGATTGCCGGTGCGACCTGCACCGA

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CGCATGAACCAAGTTCCACAACCGGTGCTCTTGCACGCAAGCTCCGCG

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GCCGTCTCGCCCGAAGCCAGCAAGCACGCAGACTACCGCGCCATCGT

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TGCTCGAATTGGCTTTGTGTCCGGCAGCGCGGCAGCAACGCTTGCAGT

GCTCCGAGCCGCCTCTGCAAAACTCAAGCAGTCGAGTGCGACGCTCG

AATGGACCCTGCTCCGCGAGGGCGTCACGTACCGCTCCGCCGCGATG

CACACTCCTGGCAGTGTCGCTGCTCTGTTTGCCGGGCAAGGCGCGCAG

TACACGCACATGTTCGCTGACGTTGCCATGAACTGGCCACCGTTTCGA

AGCGCCGTGCAAGAGATGGATGCCGCTCAAGTCACGGCGGCAGCGCC

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GCCGATGGCCCAGCCCCAAGCCTCAGCACCATCACCGTCCCCTACTGC

CTCTGTGCTGCCTAAGCCTGTTGCTTTACCAGCTAGTGTCGATCCCGCC

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GACTGGCTACGAGGTCGACATGATCGAGGCTGACATGCTGCTCGACG

CCGAGCTCGGCATCGACTCGGTCAAGCGCATTGAGATCCTGGCGGCTG

TCCAAGCTCAGCTCGGGGTCGAGGCCAAGGATGTCGACGCGCTCAGC

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CTGTTGCTGCACCAACTAGCGCCGATCCCGCCAAGCTCGCGCGCGCCG

AAGCCGTCGTCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTCG

ACATGATCGAGGCTGACATGCTGCTCGACGCCGAGCTCGGCATCGACT

CGGTCAAGCGCATTGAGATCCTGGCGGCTGTCCAAGCCCAGCTCGGG

GTCGAGGCCAAGGACGTCGACGCGCTCAGCCGCACACGCACGGTTGG

CGAGGTCGTCGAGGCCATGAAGGCTGAGATCGGCGGGCAAGCGACC

AGTGCACCTGCGTCCGTGGCCCAGCCCCAAATCTCTGTGTCCCCTACG

CCTCTCGCTGCATCTCCTAGTGCCGATCCTGCCAAGCTCGCGCGCGCC

GAAGCCGTCGTCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTC

GACATGATCGAGGCTGACATGCTGCTCGACGCCGAGCTCGGCATCGA

CTCCGTCAAGCGCATCGAGATCCTGGCGGCTGTCCAGGCCCAGCTCGG

GGTCGAGGCCAAGGACGTCGACGCGCTCAGCCGCACACGCACTGTTG

GCGAGGTCGTTGACGCCATGAAGGCTGAGATCGGCGGGCAAGCGACC

AGTGCGCCTGCATCCGTGGCCCAGCCCCAAGCCTCAGCACCGTCGCC

GTCCGCTACTGCCTCTGTGCTGCCTAAGCCTGTTGCTGCACCAACTAGC

GCCGATCCCGCCAAGCTCGCGCGCGCCGAAGCCGTCGTCATGGAGGT

TCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCGAGGCTGACAT

GCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAAGCGCATCGAGA

TCCTGGCGGCTGTCCAAGCCCAGCTCGGGGTCGAGGCCAAGGACGTC

GACGCGCTCAGCCGCACACGCACGGTTGGCGAGGTCGTCGAGGCCAT

GAAGGCTGAGATCGGCGGGCAAGCGACCAGTGCACCTGCGTCCATGG

CCCAGCCCCAAATCTCTGTGTCCCCTACGCCTCTCGCTGCATCTCCTAG

TGCCGATCCTGCCAAGCTCGCGCGCGCCGAGGCCGTCGTCATGGAGGT

TCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCGAGGCCGACA

TGCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAAGCGCATCGAG

ATCCTGGCGGCTGTCCAAGCTCAGCTCGGGGTCGAGGCCAAGGACGT

CGACGCGCTCAGCCGCACACGCACGGTTGGCGAGGTCGTTGATGCCA

TGAAGGCTGAGATCGGCGGGCAAGCGACCAGTGCGCCTGCATCCGTG

GCCCAGCCCCAAGCCTCAGCACCGTCGCCGTCCGCTACTGCCTCTGCG

CCTGTTACGCCTCTCGCTGCACCAGCTAGTGTCGATCCCGCCAAGCTC

GCGCGCGCCGAAGCCGTCGTCATGGAGGTTCTCGCCGCCAAGACTGG

CTACGAGGTCGACATGATCGAGGCTGACATGCTGCTCGACGCCGAGC

TCGGCATCGACTCCGTCAAGCGGATTGAGATCCTGGCGGCTGTCCAAG

CCCAGCTCGGGGTCGAGGCCAAGGACGTCGACGCGCTCAGCCGCACA

CGCACTGTTGGCGAGGTCGTTGACGCCATGAAGGCTGAGATCGGCGG

GCAAGCGACCAGCGCACCTGCGTCCGTGGCCCAGCCCCAAGCCTCAG

CACCGTCGCCGTCCGCTACTGCCTCTGTGCTGCCTAAGCCTGTTGCTTC

ACCAGCTAGTGTCGATCCCGCCAAGCTCGCGCGCGCCGAAGCGGTCG

TCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCG

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CGCATGAACCAAGTTCCACAACCGGTGCTCTTGCACGCAAGCTCCGCG

TCAGCTCTT

SEQ ID NO:13:

METKDDRVAIVGMSAILPCGESVRESWEAIREGLDCLQDLPADRVDITAYY

DPNRGGFIPEYDFDAREFGLNMFQMEDSDANQTVTLLKVKEALEDAGVEP

FTK

KKKNIGCVLGIGGGQKASHEFYSRLNYVVVEKVLRKMNLPDEVVEAAVEK

YKANFPEWRLDSFPGFLGNV TAGRCSNVFN

MEGMNCVVDAACASSLIAIK

VAIDELLHGDCDTMIAGATCTDNSIGMYMAFSKTPVFSTDQSVKAYDAKT

KGMLIGEGSAMVVLKRYADAVRDGDEIHAVIRACASSSDGKAAGIYAPTV

SGQEEALRRAYARAGVDPSTVTLVEGHGTGTPVGDRIELTALRNVFDAAN

KGRKETVAVG SIKSQIGHLK

AVAGFAGLVKVVMALKHKTLPQTINVHDPP

ALHDGSPIQDSSLYINTMNRPWFTAPGVPRRAGISSFGFGGANYHAVLEE

AEPEHAKPYRMNQVPQPVLLHASSASAL

SEQ ID NO:14:

CAGTCGAGTGCGACGCTCGAATGGACCCTGCTCCGCGAGGGCGTCAC

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GCCGGGCAAGGCGCGCAGTACACGCACATGTTCGCTGACGTTGCCAT

GAACTGGCCACCGTTTCGAAGCGCCGTGCAAGAGATGGATGCCGCTC

AAGTCACGGCGGCAGCGCCGAAGCGCCTCAGCGAGGTCCTGTATCCG

CGCAAGCCGTACGCTGCAGAGCCCGAGCAAGACAACAAGGCCATCTC

GATGACGATTAACTCGCAACCGGCCCTCATGGCCTGCGCTGCTGGGGC

GTTTGAGGTGTTTCGTCAAGCTGGTCTTGCGCCCGACCACGTCGCGGG

TCATTCTCTCGGCGAGTTTGGTGCTTTGCTCGCCGCTGGATGCGCAAGC

CGTGAGGAGCTCTTCCGTCTGGTCTGCAGCAGAGCGAAGGCAATGCA

AGACGTTCCCAAGCCAAGCGAGGGCGTCATGGCAGCTGTCATCGGCC

GTGGTGCTGACAAGCTCACGCTGCAAGGCGATGGTGCGTGGCTTGCCA

ACTGCAACTCGCCAAGCCAAGTGGTCATTTCCGGCGACAAGACTGCT

GTCGAGCGTGAATCCAGCCGGTTGGCAGGCCTTGGCTTCAGGATCATT
CCGCTTGCATGCGAAGGCGCCTTCCATTCACCGCACATGACGGCGGCC
CAGGCCACGTTTCAGGCTGCACTGGACAGCCTCAAGATCTCCACCCCG
ACGAACGGGGCGCGCCTGTACAACAACGTTTCCGGAAAGACCTGCCG
ATCCCTGGGTGAACTCCGCGACTGCCTGGGCAAGCACATGACAAGTC
CTGTGCTCTTCCAGGCACAGGTAGAGAACATGTACGCTGCCGGGGCG
CGCATTTTCGTGGAGTTTGGCCCGAAGCAAGTCCTCTCCAAGCTCGTA
GGCGAGATTCTCGCCGACAAGTCAGACTTTGTGACAGTCGCGGTCAAC
TCGTCATCGTCCAAGGACAGCGACGTGCAACTTCGTGAAGCTGCTGCG
AAGCTCGCGGTCCTTGGCGTCCCGTTGGCGAACTTTGACCCTTGGGAG
CTCTGCGACGCGCGGCGTCTTCGCGAATGCCCGCGATCCAAGACGAC
GTTGCGCTTGTCTGCAGCGACCTACGTGTCGAACAAGACCCTTGCTGC
TAGGGAGAAGGTCATGGAGGACAACTGCGACTTTTCTTCGCTCTTTGC
CTCCGGTCCAGCAAGCCAAGAGATGGAGCGAGAAATAGCCAACCTTC
GCGCTGAGCTGGAGGCGGCCCAACGCCAGCTTGACACGGCCAAA

SEQ ID NO:15:

QSSATLEWTLLREGVTYRSAAMHTPGSVAALFAGQGAQYTHMFADVAM
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NSQPALMACAAGAFEVFRQAGLAPDHVAGHSLGEFGALLAAGCASREEL
FRLVCSRAKAMQDVPKPSEGVMAAVIGRGADKLTLQGDGAWLANCNSP
SQVVISGDKTAVERESSRLAGLGFRIIPLACEGAFHSPHMTAAQATFQAAL
DSLKISTPTNGARLYNNVSGKTCRSLGELRDCLGKHMTSPVLFQAQVENM
YAAGARIFVEFGPKQVLSKLVGEILADKSDFVTVAVNSSSSKDSDVQLREA
AAKLAVLGVPLANFDPWELCDARRLRECPRSKTTLRLSAATYVSNKTLAA
REKVMEDNCDFSSLFASGPASQEMEREIANLRAELEAAQRQLDTAK

SEQ ID NO:16:

CAAGTCACTTCCGCTCCCATCGCCGAGCTCGCGCGCGCCGAGGCCGTC

GTCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATC

GAGGCCGACATGCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAA

GCGCATTGAGATCCTGGCAGCTGTCCAGGCCCAGCTCGGGGTCGAGG

CCAAGGACGTCGACGCGCTCAGCCGCACACGAACAGTTGGCGAGGTC

GTTGACGCCATGAAGGCTGAGATCGGCGGG

SEQ ID NO:17:

QVTSAPIAELARAEAVVMEVLAAKTGYEVDMIEADMLLDAELGIDSVKRIE

ILAAVQAQLGVEAKDVDAL SRTRTVGEVVDAMKAEIGG

SEQ ID NO:18:

CATCTCTTTGGCACGGGATGTGAAGACCTGAGCCTTTGCTCTGCTTCTG

TGGTTGAGATTGCTCGTTGCAGCGAACTAGCTCTGGAGCGCCCGATGG

ATCGGCCCATTCTTATTGTAAGCGATGGATCAGCATTGCCGGCGGCTC

TGGCTAGTCGACTGGGGTCGTGTGCAGTAATCCTCACGACCGCAGGCG

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AGCTAGGGACCAGCTTGGCTTTGCCCTGCTGCTTGCCAAGCATTCGAG

CAAAGCGCTCAACCAGCAGATCCCAGGCGGGCGCGCCTGCTTCGTGG

GCGTCTCGCGAATCGACGGAAAGCTCGGACTTAGCGGAGCTTGCGCG

AAAGGAAAGGGCTGGGCTGAGGCCGCAGAGATTGCTCAGCAAGGAG

CCGTCGCGGGCTTGTGCAAGACCTTGGACCTAGAGTGGCCGCACGTCT

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GACCGGTTGGGCTTGGCAAGCCCAAGCAGGCACTACGTTCTTCGGAC

GTCTTCTTGGTTTCTGGTGGGGCGCGGGGAATTACACCTGTTTGCGTTC

GCGAGTTGGCCAAATCGATCAGTGGTGGCACTTTTGTCCTCCTCGGGC

GGTCCCCTCTCGCTGATGATCCGGCGTGGGCTTGCGGCGTCGAGGAAG

CAAACATTGGGACAGCCGCTATGGCGCACCTCAAGGCCGAGTTCGCA

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GGGGCTGTAACTGGGGTTGTGCACGCCTCTGGTGTTCTCCGAGACAAG

TCCGTTGAGCGCTTGGAGCTCGCCGACTTCGAGGTCGTGTACGGCACC

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ACTGGGCAGGCCGTGTACGCTATGGCGAATGAGGCGCTGAACAAGAT

GGCCTTCCATTTGGAAACTGCGATGCCTGGCCTCTCGGTCAAGACGAT

CGGGTTTGGACCTTGGGACGGCGGCATGGTCAACGATGCGCTGAAAG

CGCACTTTGCGTCTATGGGCGTCCAAATTATTCCGCTCGACGGCGGCG

CGGAGACCGTTTCCCGAATCATCGGGGCGTGCTCGCCAACACAAGTTC

TGGTTGGCAACTGGGGCTTGCCCCCTGTAGTTCCTAACGCGAGCGTGC

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5   GANEETAA

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AMAHLKAEFAAGRGPKPTPKAHKALVGSVLGAREVLGSLESIRAQGARA

E

10   YVSCDVSCAERVKAVVDDLERRVGAVTGVVHASGVLRDKSVERLELADFE

VVYGTKVDGLLNLLQAVDRPKLRHLVLFSSLAGFHGNTGQAVYAMANE

AL

NKMAFHLETAMPGLSVKTIGFGPWDGGMVNDALKAHFASMGVQIIPLDG

G

15   AETVSRIIGACSPTQVLVGNWGLPPVVPNASVHKITVRLGGESANPFLSS

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T

CEVQLRRESSTASPSEVVLSASLNVFAAGKVVPAYRAHVVLGASGPRTGG

VQLELKDLGVDADPACSVGKGALYDGRTLFHGPAFQYMDEVLRCSPAEL

20   A

VRCRVVPSAAQDRGQFVSRGVLYDPFLNDTVFQALLVWARLVRDSASLPS

NVERISFHGQPPSEGEVFYTTLKLDSAASGPLDPIAKAQFFLHRACGAVF

ASGRASVVLNKALSF

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AGAAGAGCACTATGCGCCCGAGAGGTCAAAGTACGCCGATACGTTCTGC

AACGAGAGGTACGGATGCATCGATCCCAAAGTCGACAACGAGCACGAC

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CTTCGGACACACCCTCGTCGCGGCCGGCTTTGCGGGAATGTGCAAGGTTC

TCCTTGCAATGGAGCGCGGCGTGATCCCCCCGACCCCGGGCGTTGACTCT

GGCACCCAGATTGATCCCCTCGTCGTCACAGCGGCGCTCCCGTGGCCGGA
TACGCGCGGCGGGCCGAAACGCGCAGGACTCTCCGCATTCGGATTCGGG
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SEQ ID NO: 21:

MNQGGRNDEGVSVARADPCPDTRIAVVGMAVEYAGCRGKEAFWDTLMNG
KINSACISDDRLGSARREEHYAPERSKYADTFCNERYGCIDPKVDNEHDLLLG
LAAAALQDAQDRRSDGGKFDPAQLKRCGIVSGCLSFPMDNLQGELLNLYQA
HAERRIGKHCFADQTPWSTRTRALHPLPGDPRTHRDPASFVAGQLGLGPLHY
SLDAACASALYVLRLAQDHLLSGEADLMLCGATCFPEPFFILTGFSTFHAMPV
GENGVSMPFHRDTQGLTPGEGGSVMVLKRLADAERDGDHIYGTLLGASLSN
AGCGLPLKPHQPSEEACLKATYELVGVPPRDVQYVECHATGTPQGDTVELQA
VKACFEGASPRIGSTKGNFGHTLVAAGFAGMCKVLLAMERGVIPPTPGVDSG
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SEQ ID NO: 22:

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GCTTCTTGGGCGGGGACGAGTCCTTTCTCCACGAGATCGGACTCGAGTGC
TCTCCGCACGGGTGCTACATTGAGGACGTGGATGTGGACTTTAAGCGACT
CCGCACGCCAATGGTGCCGGAGGACTTGCTCCGGCCGCAACAGCTCCTG
GCCGTGTCGACGATTGACAAGGCCATCCTCGACTCGGGCTTGGCCAAGG
GCGGCAACGTGGCTGTCCTTGTCGGCCTCGGGACGGACCTCGAGCTCTAC
CGCCACCGAGCTCGGGTTGCGCTTAAGGAGCGTCTTCAAGGACTGGTTCG
CTCTGCCGAGGGAGGAGCCCTGACGTCTCGCCTGATGAACTATATCAATG
ATAGCGGAACGTCGACCTCCTACACGTCGTATATCGGCAACCTCGTCGCC
ACGCGCGTCTCGTCCCAGTGGGGCTTCACTGGGCCGTCGTTCACCGTCAC
GGAAGGGGCCAACTCGGTCCATCGGTGCGCCCAGCTCGCCAAGTACATG

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CGGGAGCGCCGAGGCGTTCTTCGTGAGGTCGCGCCGCATGCAGATCTCGA

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GCCGCTGCCCTCGTAAAAACTGCGCTCTGCTTGCACAACCGCTACTTGGC

GGCTACCCCAGGCTGGGATGCGCCTGCTGCCGGCGTGGATTTTGGTGCCG

AGCTGTACGTTTGCCGCGAGTCGCGTGCTTGGGTCAAGAACGCCGGCGTT

GCACGGCACGCCGCAATTTCTGGCGTGGACGAAGGCGGGTCG

SEQ ID NO:23:

QPRLGSGPNRKLAIVGMDATFGSLKGLSALEAALYEARHAARPLPAKRWRFL

GGDESFLHEIGLECSPHGCYIEDVDVDFKRLRTPMVPEDLLRPQQLLAVSTIDK

AILDSGLAKGGNVAVLVGLGTDLELYRHRARVALKERLQGLVRSAEGGALTS

RLMNYINDSGTSTSYTSYIGNLVATRVSSQWGFTGPSFTVTEGANSVHRCAQL

AKYMLDRGEVDAVVVAGVDLCGSAEAFFVRSRRMQISKSQRPAAPFDRAAD

GFFAGEGCGALVFKRLTDCVSGERIYASLDSVVVATTPRAALRAAAGSARVDP

ASIDMVELSADSHRFVRAPGTVAQPLTAEVEVGAVREVIGTAGRGSRSVAVGS

VRANVGDAGFASGAAALVKTALCLHNRYLAATPGWDAPAAGVDFGAELYV

CRESRAWVKNAGVARHAAISGVDEGGS

SEQ ID NO:24:

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TCGGCGAGTCGCTCGTCGGTTGCGCGGCTGGCAGCGGCGGGCTGACCCTT

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AVEFNALRKLWGVAPGAPVDSFWQGYVVRATRAQVEQAIGEDNQFVRLLIV

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MLRFPSQDETGGCKMYSSVSNSRIGPVEESQMGPGTELVFSPSMEDFVAQLYSR

VADFPAITEAVYQQGHDVFVEVGPDHSRSAAVRSTLGPTRRHIAVAMDRKGE

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GAGCGGCACACGGCGTCGATTATGCGCTCTACATGGGCGCAATGGCCAA

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TGCGGGGGGCGGTTTCCTTGCGTTGTGCGCGTTAACCAGGAGATATTATG

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GGGAAAGCGCGGACGCGTTGGCGTACACGGTTGCGGAAGCCAGATAG

SEQ ID NO:27:

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ALYMGAMAKGVASAEMVIAAGKARMLASFGAGGLPLGEVEEALDKIQAALP

EGPFAVNLIHSPFDPNLEEGNVELFLRRGIRLVEASAFMSVTPSLVRYRVAGLE

RGPGGTARVLNRVIGKVSRAELAEMFMRPPPAAIVSKLLAQGLVTEEQASLAE

IVPLVDDVAIEADSGGHTDNRPIHVVLPVVLALRDRVMRECKYPAANRVRVG

AGGGIGCPAAARAAFDMGAAFVLTGSINQLTRQAGTSDSVRAALARATYSDV

TMAPAADMFDQGVKLQVLKRGTMFPARANKLYELFTTYQSLDAIPRAELARL

EKRVFRMSIDEVWNETKQFYETRLNNPAKVARAERDPKLKMSLCFRWYLSKS

SKWASTGQVGRELDYQVWCGPTIGAFNEFVKGSSLDAEACGGRFPCVVRVN

QEILCGAAYEQRLARFMLLAGRESADALAYTVAEAR